

# SEQUENCE LISTING

<110> Young, Karen K. Y.

<120> Compositions and Methods for Detecting Certain  
Flaviviruses, Including Members of the Japanese  
Encephalitis Virus Serogroup

<130> 022101-000230US

<140> US 10/815,480

<141> 2004-03-31

<150> US 60/459,491

<151> 2003-03-31

<150> US 60/552,454

<151> 2004-03-12

<150> US 60/555,530

<151> 2004-03-22

<160> 919

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region of the genomes of flaviviruses

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25

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<220>

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25

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<220>

<223> Japanese encephalitis virus serogroup Primer 1

<220>  
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 gaaagcctcc cagamccgty tcggaa 26  
  
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 sequence in 3' untranslated region of the genome  
 of Japanese encephalitis virus serogroup, KY1129

<400> 7  
 gtaagccctc agaaccgtct cggaa 25  
  
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 <212> DNA  
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 serogroup amplification primer  
  
 <400> 8  
 gtaagccctc agaaccgtct cggaa 25  
  
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 region of the genomes of flaviviruses, consensus  
 sequence  
  
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 tctcctagtc tatcccaggt gtcaa 25  
  
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 <222> (11)...(11)  
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 yccyastmtw nyccaggtr tcaa 24  
  
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<220>  
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 ycctagtcta tcccaggtrt caa 23  
  
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 cccyastmta tyyccagggtg tcaa 24  
  
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 <210> 15  
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 <223> Example Primer 2, Japanese encephalitis virus serogroup  
 amplification primer, region of conserved sequence in 3'  
 untranslated region of the genome of Japanese encephalitis  
 virus serogroup, KY1129  
  
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 tcctagtcta tcccagggtgt caa 23  
  
 <210> 16  
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 <223> region of conserved sequence in 3' untranslated  
 region of the genome of flaviviruses, KY1129  
  
 <400> 16  
 ggactagagg ttagaggaga ccccgcg 28  
  
 <210> 17  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> complement to SEQ ID NO:16

<400> 17  
 ccgcgggggtc tcctctaacc tctagtcc 28

<210> 18  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> probe for detecting flaviviruses, oligonucleotide  
 that hybridizes to conserved region of flaviviral  
 nucleic acid

<220>  
 <221> modified\_base  
 <222> (25)...(25)  
 <223> n = g, c, t, a or absent

<220>  
 <221> modified\_base  
 <222> (26)...(26)  
 <223> n = c, t, g or absent

<220>  
 <221> modified\_base  
 <222> (27)...(28)  
 <223> n = g, c, a, t or absent

<400> 18  
 ggwctagwgg ttagaggaga ccynnnnn 28

<210> 19  
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 <212> DNA  
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<220>  
 <223> probe for detecting Japanese encephalitis virus  
 serogroup members

<400> 19  
 ggactagwgg ttagaggaga ccccrykk 28

<210> 20  
 <211> 28  
 <212> DNA  
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<220>  
 <223> probe for detecting West Nile virus

<400> 20  
 ggactagwgg ttagaggaga cccrcgk 28

<210> 21  
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 <212> DNA  
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<220>  
 <223> probe for detecting Japanese encephalitis virus

<400> 21  
 ggactagagg ttagaggaga ccccgygg 28  
  
 <210> 22  
 <211> 28  
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 <220>  
 <223> probe for detecting Murray Valley encephalitis  
 virus  
  
 <400> 22  
 ggactagagg ttagaggaga cccactc 28  
  
 <210> 23  
 <211> 29  
 <212> DNA  
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 <220>  
 <223> probe for detecting Kunjin virus  
  
 <400> 23  
 aataygtgga ttacatgast tcaytgaag 29  
  
 <210> 24  
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 <212> DNA  
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 <223> probe for detecting Dengue virus  
  
 <400> 24  
 ggactagagg ttagaggaga ccccyssv 28  
  
 <210> 25  
 <211> 28  
 <212> DNA  
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 <220>  
 <223> probe for detecting yellow fever virus  
  
 <400> 25  
 ggtctagagg ttagaggaga ccctccag 28  
  
 <210> 26  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> probe for detecting Montana myotis  
 leukencephalitis virus  
  
 <400> 26  
 ggactagagg ttagaggaga ccccttcc 28

<210> 27  
<211> 28  
<212> DNA  
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<220>  
<223> probe for detecting Modoc virus

<400> 27  
ggactagagg ttgagggaga cccccggc 28

<210> 28  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Example Probe 1, Japanese encephalitis virus  
serogroup amplification primer

<400> 28  
ggactagagg ttagaggaga cccccgcg 28

<210> 29  
<211> 418  
<212> DNA  
<213> St. Louis encephalitis virus

<220>  
<223> 3' untranslated region of the genome of St. Louis  
encephalitis virus (SLEV) isolate BFS1750

<400> 29  
ttgccaccgg atgtcaggta aacgggtgctg tctgtaacct ggccccaggt gactgggtta 60  
tcaaagccaa tctggccgag tgcaaagccc ctcatccga ctcgaggagg tccctagcac 120  
gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180  
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgcaac 300  
ttggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360  
agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 30  
<211> 342  
<212> DNA  
<213> St. Louis encephalitis virus

<220>  
<223> 3' untranslated region of the genome of St. Louis  
encephalitis virus (SLEV) isolate 1750-Std

<400> 30  
ttgccaccgg atgtcaggta aacgggtgctg tctgtaacct ggccccaggt gactgggtta 60  
tcaaagccaa tctggccgag tgcaaagccc ctcatccga ctcgaggagg tccctagcac 120  
gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180  
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgcgcaact 300  
tggcaaggcc caaaccgct cgaagctgta gagacggggg aa 342

<210> 31  
<211> 418  
<212> DNA  
<213> St. Louis encephalitis virus

<220>  
<223> 3' untranslated region of the genome of St. Louis  
encephalitis virus (SLEV) isolate TD6-4G

<400> 31  
ttgccaccgg atgtcaggta aacggtgctg cctgtaacct ggccccaggt gactgggtta 60  
tcaaagccaa tctggccgag tgcaaagccc ctcatgccga ctcgaggagg tccctggcac 120  
gtaggctgga gaggacgcaa aagtcagacc agaaatgccca cctgaaagca tgctaaaggt 180  
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgcaac 300  
tcggcaaggc ccaaaccgcg tcgaagctgt agagatgggg gaaggactag aggttagagg 360  
agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 32  
<211> 342  
<212> DNA  
<213> St. Louis encephalitis virus

<220>  
<223> 3' untranslated region of the genome of St. Louis  
encephalitis virus (SLEV) isolate CoaV750

<400> 32  
ttgccaccgg atgtcaggta aacggtgctg cctgtaacct ggccccaggt gactgggtta 60  
ccaaagccaa tctggctgag tgcaaagccc ctcggtccga ttcgggaggg tccctggcac 120  
gtaggctgga gaggacgcaa aagtcagacc agaaatgccca cctgaaagca tgctaaaggt 180  
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgcgcaact 300  
tggcaaggcc aaaaccgcgt cgaagctgta gagatggggg aa 342

<210> 33  
<211> 418  
<212> DNA  
<213> St. Louis encephalitis virus

<220>  
<223> 3' untranslated region of the genome of St. Louis  
encephalitis virus (SLEV) isolate L695121.05

<400> 33  
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tcaaagccaa tccggctggg tgcaaagccc ctcatgccga ctcgaggagg tccctggcat 120  
gtaggctgga gaggacgcaa aagtcagacc agaaatgccca cctgaaagca tgctaaaggt 180  
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaac 300  
ttggcaaggc ccaaaccgcg tcgaagctgt agagacgggg gaaggactag aggttagagg 360  
agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 34  
<211> 418  
<212> DNA  
<213> St. Louis encephalitis virus



<220>  
 <223> 3' untranslated region of the genome of St. Louis  
 encephalitis virus (SLEV) isolate TNM771K

<220>  
 <221> modified\_base  
 <222> (384)...(384)  
 <223> n = g, a, c or t

<400> 34  
 ttgccaccgg atgtcaggta aacgggtgctg tctgtaacct ggccccaggt gactgggtca 60  
 tcaaagccaa tctggctggg tgcaaagccc ctcatgccga ctcgggaggg tccctggcac 120  
 gtaggctgga gaggacgcac aagtcagacc agaaatgcc cctgaaagca tgctaaaggt 180  
 gctgtctgta catgcccac gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
 aaccatggag agcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaac 300  
 ttggcaaggc ccaaaccgc tcgaagctgt agagacggg gaaggactag aggttagagg 360  
 agacccttg ccgttaacgc aaanaacagc atattgacac ctggaaagac aggagatc 418

<210> 35  
 <211> 418  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> 3' untranslated region of the genome of St. Louis  
 encephalitis virus (SLEV) isolate MSI-7

<400> 35  
 ttgccaccgg atgtcaggta aacgggtgctg tctgtaacct ggccccaggc gactgggtta 60  
 tcaaagccaa tccggctggg tgcaaagccc ctcatgccga ctcgggaggg tccctggcac 120  
 gtaggctgga gaggacgcac aagtcagacc agaaatgcc cctgaaagca tgctaaaggt 180  
 gctgtctgta catgcccac gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
 aaccatggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaac 300  
 ttggcaaggc ccaaaccgc tcaaagctgt agagacggg gaaggactag aggttagagg 360  
 agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 36  
 <211> 405  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> 3' untranslated region of the genome of St. Louis  
 encephalitis virus (SLEV) isolate Kern217

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 ccgcatgtca ggtaaaccgt gctgtctgta acctggcccc aggtcactgg gttatcaaag 60  
 ccaaccggc tgggtgcaaa gcccctcatt ccgactcggg aggggccctg gcacgtaggc 120  
 tggagaggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180  
 tgtacatgcc ccaggaggac tgggttaaca aagcttaaca gccccagcgg cccaaaccat 240  
 ggagtgcgtg accatggcgt aaggactaga ggttagagga gacccgctg taacttggca 300  
 aggcccaaac ccgctcaaag ctgtagagac gggggaagga ctagagggtta gaggagaccc 360  
 cttgccgtta acgcaaaca cagcatattg acacctggaa agaca 405

<210> 37  
 <211> 375  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> 3' untranslated region of the genome of St. Louis  
 encephalitis virus (SLEV) isolate CoaV608

<400> 37  
 cccaggcgac tgggttatca aagccaatcc ggctgggtgc aaagcccctc attccgactc 60  
 gggaggggtcc ctggcacgta ggctggagag gacgcacaag tcagaccaga aatgccacct 120  
 gaaagcatgc taaagggtgct gtctgtacat gccccaggag gactgggtta acaaagctta 180  
 acagccccag cggcccaaac catggagtgc gtgaccatgg cgtaaggact agagggttaga 240  
 ggagaccccg ctgtaacttg gcaaggccca aaccgctca aagctgtaga gacgggggaa 300  
 ggactagagg ttagaggaga ccccttgccg ttaacgcaaa caacagcata ttgacacctg 360  
 gaaagacagg agatc 375

<210> 38  
 <211> 411  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> 3' untranslated region of the genome of St. Louis  
 encephalitis virus (SLEV) isolate TBH-28

<400> 38  
 ttgccaccgg atgtcaggta aacgggtgctg tctgtaacct ggccccagggt gactgggtta 60  
 tcaaagccaa cccggctggg tgcaaagccc ctcatccga ctcgaggagg tccctggcac 120  
 gtaggcgga gaggacgcac aagtcagacc agaaatgcca cctgaaagca tgctaaagggt 180  
 gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
 aacctggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaat 300  
 ttggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360  
 agacccttg ccgttaacgc aaacaacagc atattgacac ctggaagac a 411

<210> 39  
 <211> 402  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
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 encephalitis virus (SLEV) isolate VR1265

<400> 39  
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 ccaatctggc tgggtgcaaa gcccctcatt ccgactcggg agggtccttg gcacgtaggc 120  
 tggagcggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180  
 tgtacatgcc ccaggaggac tgggttaaca aagcttaaca gccccagcgg cccaaacct 240  
 ggagtgcgtg accatggcgt aaggactaga ggtagagga gaccccgctg taacttggca 300  
 aggcccaaac ccgctcgaag ctgtagagac gggggaagga ctagaggta gaggagacc 360  
 cttgccgtca acgcaacaa cagcatattg acacctggaa ag 402

<210> 40  
 <211> 374  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> 3' untranslated region of the genome of St. Louis  
 encephalitis virus (SLEV) isolate CoaV353

<400> 40  
 cccaggtgac tgggttatca aagccaatct agctgagtgc aaagcccctc attccgactc 60  
 gggaggggtcc ctggcacgta ggctggagag gacgcaaaag tcagaccaga aatgccacct 120  
 gaaagcatgc taaaggtgct gtctgtacat gccccaggag gactgggtta acaaagctta 180  
 acagccccag cggcccaaac catggagtgc gtgaccatgg cgtaaggact agagggttaga 240  
 ggagaccccc ctgcaacttg gcaaggccca aaccgcctcg aagctgtaga gacgggggaa 300  
 ggactagagg ttagaggaga ccccttgccg ttaacgcaa caacagcata ttgacacctg 360  
 gaaagacagg agat 374

<210> 41  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Dengue virus consensus upstream primer

<400> 41  
 gagccccgtc caaggacgta aaaagaa 27

<210> 42  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Dengue virus consensus upstream primer

<220>  
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 <222> (27)...(27)  
 <223> n = t-butyl-benzyl-dA

<400> 42  
 gagccccgtc caaggacgta aaaagan 27

<210> 43  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Dengue virus consensus upstream primer

<220>  
 <221> modified\_base  
 <222> (26)...(26)  
 <223> n = methyl-dA

<220>  
 <221> modified\_base  
 <222> (27)...(27)  
 <223> n = t-butyl-benzyl-dA

<400> 43  
 gagccccgtc caaggacgta aaaagnn 27

<210> 44  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Dengue virus type I upstream primer  
  
 <400> 44  
 gagccccgta caaggacgta aaatgaa 27  
  
 <210> 45  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Dengue virus type I upstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (27)...(27)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 45  
 gagccccgta caaggacgta aaatgan 27  
  
 <210> 46  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Dengue virus type I upstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (26)...(26)  
 <223> n = methyl-dA  
  
 <220>  
 <221> modified\_base  
 <222> (27)...(27)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 46  
 gagccccgta caaggacgta aaatggn 27  
  
 <210> 47  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Dengue virus types II and III upstream primer  
  
 <400> 47  
 gagccccgta caaggacgtt aaaagaa 27  
  
 <210> 48  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Dengue virus types II and III upstream primer

<220>  
 <221> misc\_feature  
 <222> (27)...(27)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 48  
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 <210> 49  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Dengue virus types II and III upstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (26)...(26)  
 <223> n = methyl-dA  
  
 <220>  
 <221> modified\_base  
 <222> (27)...(27)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 49  
 gagccccgtc caaggacggtt aaaagnn 27  
  
 <210> 50  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Dengue virus type IV upstream primer  
  
 <400> 50  
 attgaagtca ggccacttgt gcca 24  
  
 <210> 51  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Dengue virus type IV upstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (24)...(24)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 51  
 attgaagtca ggccacttgt gccn 24  
  
 <210> 52  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Dengue virus type IV upstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (23)...(23)  
 <223> n = ethyl-dC  
  
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 <221> modified\_base  
 <222> (24)...(24)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 52  
 attgaagtca ggccacttgt gcnn 24  
  
 <210> 53  
 <211> 25  
 <212> DNA  
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 <223> Dengue virus downstream primer  
  
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 gatctctggt ctttcccagc gtcaa 25  
  
 <210> 54  
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 <223> Dengue virus downstream primer  
  
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 <221> modified\_base  
 <222> (25)...(25)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 54  
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 <210> 55  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Dengue virus downstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (24)...(24)  
 <223> n = methyl-dA  
  
 <220>  
 <221> modified\_base  
 <222> (25)...(25)  
 <223> n = t-butyl-benzyl-dA

<400> 55  
 gatctctggt ctttcccagc gtcnn 25  
  
 <210> 56  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> yellow fever virus upstream primer  
  
 <400> 56  
 aaccgggata aaaactacgg gtggagaa 28  
  
 <210> 57  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> yellow fever virus upstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (28)...(28)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 57  
 aaccgggata aaaactacgg gtggagan 28  
  
 <210> 58  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> yellow fever virus upstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (27)...(27)  
 <223> n = methyl-dA  
  
 <220>  
 <221> modified\_base  
 <222> (28)...(28)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 58  
 aaccgggata aaaactacgg gtggagnn 28  
  
 <210> 59  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> yellow fever virus upstream primer  
  
 <400> 59  
 ataaaaacta cgggtggaga accgga 26

<210> 60  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> yellow fever virus upstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (26)...(26)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 60  
 ataaaaacta cgggtggaga accggn 26  
  
 <210> 61  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> yellow fever virus downstream primer  
  
 <400> 61  
 actccggtct ttccctggcg tcaa 24  
  
 <210> 62  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> yellow fever virus downstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (24)...(24)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 62  
 actccggtct ttccctggcg tcan 24  
  
 <210> 63  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> yellow fever virus downstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (23)...(23)  
 <223> n = methyl-dA  
  
 <220>  
 <221> modified\_base  
 <222> (24)...(24)  
 <223> n = t-butyl-benzyl-dA



<400> 63  
 actccggtct ttccctggcg tcnn 24  
  
 <210> 64  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> St Louis encephalitis virus upstream primer  
  
 <400> 64  
 caaagcccct cattccgact cggga 25  
  
 <210> 65  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> St Louis encephalitis virus upstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (25)...(25)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 65  
 caaagcccct cattccgact cgggn 25  
  
 <210> 66  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> St Louis encephalitis virus downstream primer  
  
 <400> 66  
 tctcctgtct ttccaggtgt caa 23  
  
 <210> 67  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> St Louis encephalitis virus downstream primer  
  
 <220>  
 <221> modified\_base  
 <222> (23)...(23)  
 <223> n = t-butyl-benzyl-dA  
  
 <400> 67  
 tctcctgtct ttccaggtgt can 23  
  
 <210> 68  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> St. Louis encephalitis virus (SLEV) first primer complement

<400> 68  
 ttgacacctg gaaagacagg aga 23

<210> 69  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> St. Louis encephalitis virus (SLEV) second primer

<400> 69  
 caaagcccct cattccgact cggg 24

<210> 70  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> flavivirus anti-sense probe

<400> 70  
 ggggtctctc taacctctag tccttcccc 30

<210> 71  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF196835 region of conserved sequence in 3' untranslated region

<400> 71  
 caaccccgagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 72  
 <211> 105  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF196835 region of conserved sequence in 3' untranslated region

<400> 72  
 tgactgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 73  
 <211> 121  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF196835 region of conserved sequence in 3' untranslated region

<400> 73  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60  
 gactgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120  
 a 121

<210> 74  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Example Primer 2, Japanese encephalitis virus serogroup amplification primer

<400> 74  
 tctcctagtc tatcccaggt gtcaa 25

<210> 75  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> detectably-labeled oligonucleotide

<220>  
 <221> modified\_base  
 <222> (1)...(1)  
 <223> n = g attached to 3' of deoxyribose phosphate backbone modified by 6-carboxyfluorescein (FAM) (I) attached to 3' of oligonucleotide 5'GGTCTAGA3', where 5' G is modified by Cy5 quencher (F)

<400> 75  
 ngttagagga gaccctccag 20

<210> 76  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fluorescent moiety-quencher moiety pair in probe variant of SEQ ID NO:28

<220>  
 <221> modified\_base  
 <222> (1)...(1)  
 <223> n = g attached to 3' of deoxyribose phosphate backbone modified by 6-carboxyfluorescein (FAM) (I) attached to 3' of oligonucleotide 5'GGACTAGA3', where 5' G is modified by Cy5 quencher (F)

<220>  
 <221> modified\_base  
 <222> (20)...(20)  
 <223> n = phosphorylated g

<400> 76  
 ngttagagga gaccccgcn 20

<210> 77  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fluorescent moiety-quencher moiety pair in probe  
 variant of SEQ ID NO:28

<220>  
 <221> modified\_base  
 <222> (1)...(1)  
 <223> n = g attached to 3' of deoxyribose phosphate backbone  
 modified by 6-carboxyfluorescein (FAM) (I) attached to 3'  
 of oligonucleotide 5'GGA-5-methyl-dC-propynyl-dU-AGA3',  
 where 5' G is modified by Cy5 quencher (F)

<220>  
 <221> modified\_base  
 <222> (3)...(4)  
 <223> n = propynyl-dU

<220>  
 <221> modified\_base  
 <222> (13)...(18)  
 <223> n = 5-methyl-dC

<220>  
 <221> modified\_base  
 <222> (20)...(20)  
 <223> n = phosphorylated g

<400> 77  
 ngnnagagga gannnngn 20

<210> 78  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fluorescent moiety-quencher moiety pair in probe  
 variant of SEQ ID NO:70

<220>  
 <221> modified\_base  
 <222> (1)...(1)  
 <223> n = t attached to 3' of deoxyribose phosphate backbone  
 modified by 6-carboxyfluorescein (FAM) (I) attached to 3'  
 of oligonucleotide 5'GGGTCTCC3', where 5' G is modified by  
 Cy5 quencher (F)

<220>  
 <221> modified\_base  
 <222> (22)...(22)  
 <223> n = phosphorylated c

<400> 78  
 nctaacctct agtccttccc cn 22

<210> 79  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fluorescent moiety-quencher moiety pair in probe  
 variant of SEQ ID NO:70

<220>  
 <221> modified\_base  
 <222> (1)...(1)  
 <223> n = propynyl-dU attached to 3' of deoxyribose phosphate backbone  
 modified by 6-carboxyfluorescein (FAM) (I) attached to 3' of  
 oligonucleotide 5'GGG-propynyl-dU-5-methyl-dC-propynyl-dU-5-methyl-  
 dC-5-methyl-dC3', where 5' G is modified by Cy5 quencher (F)

<220>  
 <221> modified\_base  
 <222> (2)...(2)  
 <223> n = 5-methyl-dC

<220>  
 <221> modified\_base  
 <222> (3)...(3)  
 <223> n = propynyl-dU

<220>  
 <221> modified\_base  
 <222> (22)...(22)  
 <223> n = phosphorylated c

<400> 79  
 nnnaacctct agtccttccc cn 22

<210> 80  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> fluorescent moiety-quencher moiety pair in probe  
 variant of SEQ ID NO:25

<220>  
 <221> modified\_base  
 <222> (1)...(1)  
 <223> n = g attached to 3' of deoxyribose phosphate backbone  
 modified by 6-carboxyfluorescein (FAM) (I) attached to 3'  
 of oligonucleotide 5'GGTCTAGA3', where 5' G is modified by  
 Cy5 quencher (F)

<220>  
 <221> modified\_base  
 <222> (20)...(20)  
 <223> n = phosphorylated g

<400> 80  
 ngtttagagga gaccctccan 20

<210> 81  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF260968 region of  
 conserved sequence in 3' untranslated region

<400> 81  
 caaccccagg aggactgggt gaacaaagct gcgagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 82  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF260969 region of  
 conserved sequence in 3' untranslated region

<400> 82  
 caaccccagg aggactgggt gaacaaagcc gcgagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 83  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF481864 region of  
 conserved sequence in 3' untranslated region

<400> 83  
 caaccccagg aggactgggt gaacaaagcc gcgagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 84  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain M12294 region of  
 conserved sequence in 3' untranslated region

<400> 84  
 caaccccagg aggactgggt gaccaaagct gcgagtgat ccacgtaagc cctcagaacc 60  
 gtctcggaag gaggacccca cgtgctttag cctcaaag 98

<210> 85  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF206518 region of  
 conserved sequence in 3' untranslated region

<400> 85  
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 86  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF317203 region of  
 conserved sequence in 3' untranslated region

<400> 86  
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 87  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF202541 region of  
 conserved sequence in 3' untranslated region

<400> 87  
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 88  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF404757 region of  
 conserved sequence in 3' untranslated region

<400> 88  
 caaccccagg aggactgggt gaacaaagcc gtgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 89  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF404753 region of  
 conserved sequence in 3' untranslated region

<400> 89  
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 90  
 <211> 98  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF404754 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 90  
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98  
  
 <210> 91  
 <211> 98  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF404755 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 91  
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98  
  
 <210> 92  
 <211> 98  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF404756 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 92  
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98  
  
 <210> 93  
 <211> 98  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF017254 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 93  
 caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98  
  
 <210> 94  
 <211> 98  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain L48977 region of  
       conserved sequence in 3' untranslated region



<400> 94  
 caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60  
 gtctcggaag caggacccca cgtgcttttag cctcaaag 98

<210> 95  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF196536 region of  
 conserved sequence in 3' untranslated region

<400> 95  
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 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 96  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF196537 region of  
 conserved sequence in 3' untranslated region

<400> 96  
 caaccccagg aggactgggt gaacaaagct gcgagcgat ccatgtaagc cctcagaacc 60  
 gtctcggaag taggacccca catgttgtag ctccaaag 98

<210> 97  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF196538 region of  
 conserved sequence in 3' untranslated region

<400> 97  
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 gtctcggaag taggacccca catgttgtag ttccaaag 98

<210> 98  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF196540 region of  
 conserved sequence in 3' untranslated region

<400> 98  
 caaccccagg aggactgggt gaacaaagct gcgagcgat ccatgtaagc cctcagaacc 60  
 gtctcggaag taggacccca catgttgtag ttccaaag 98

<210> 99  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

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<220>
<223> West Nile virus strain AF196541 region of
      conserved sequence in 3' untranslated region

<400> 99
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaaag                               98

<210> 100
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF196542 region of
      conserved sequence in 3' untranslated region

<400> 100
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaaag                               98

<210> 101
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF196543 region of
      conserved sequence in 3' untranslated region

<400> 101
caaccccagg aggactgggt taccaaagcc gcgaggtgat ccacgtaagc cctcagaacc 60
gtctcggaag gaggacccca cgtgttttag cctcaagg                               98

<210> 102
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF297840 region of
      conserved sequence in 3' untranslated region

<400> 102
caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60
gcctcggaag gaggacccca catgttgtag cttcaagg                               98

<210> 103
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF458343 region of
      conserved sequence in 3' untranslated region

<400> 103
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc ccccagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaagg                               98

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<210> 104  
 <211> 98  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF458344 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 104  
 caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98  
  
 <210> 105  
 <211> 98  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF458347 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 105  
 caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98  
  
 <210> 106  
 <211> 98  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF458348 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 106  
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98  
  
 <210> 107  
 <211> 98  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF458350 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 107  
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98  
  
 <210> 108  
 <211> 98  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF458352 region of  
       conserved sequence in 3' untranslated region

<400> 108  
 caaccccagg aggactgggt gaacaaagct gcggagcgat ccatgtaagc cctcagaacc 60  
 gcctcggaag taggacccca catgttgtag ttycaaag 98

<210> 109  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF458353 region of  
 conserved sequence in 3' untranslated region

<400> 109  
 caaccccagg aggactgggt gaacaaagct gcggagcgat ccatgtaagc cctcagaacc 60  
 gtctcggaag taggacccca catgttgtag ttccaaag 98

<210> 110  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF458355 region of  
 conserved sequence in 3' untranslated region

<400> 110  
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 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 111  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF458358 region of  
 conserved sequence in 3' untranslated region

<400> 111  
 caaccccagg aggactgggt taccaaagcc gcgaggtgat ccacgtaagc cctcagaacc 60  
 gtctcggaag gaggacccca cgtgttttag cctcaagg 98

<210> 112  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF458360 region of  
 conserved sequence in 3' untranslated region

<400> 112  
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 113  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF458361 region of  
 conserved sequence in 3' untranslated region

<400> 113  
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 114  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF208017 region of  
 conserved sequence in 3' untranslated region

<400> 114  
 caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca cgtgcttttag cctcaaag 98

<210> 115  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF196539 region of  
 conserved sequence in 3' untranslated region

<400> 115  
 caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60  
 gtctcggaag gaggaccca cgtgcttttag cctcaaag 98

<210> 116  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
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<220>  
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<210> 187  
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<220>  
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<210> 188  
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 <220>  
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 cgtctcggaa gtaggtccct gtcactgga agttgaaag 99  
  
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 <220>  
 <223> Japanese encephalitis virus strain D90194 region  
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<400> 192  
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<210> 193  
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<220>  
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<210> 194  
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<220>  
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<210> 195  
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<210> 196  
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<220>  
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<210> 197  
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<220>  
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<400> 197  
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<210> 198  
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 <212> DNA  
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<220>  
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<400> 198  
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<220>  
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<220>  
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<210> 201  
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<220>  
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<210> 202  
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 <212> DNA  
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 <220>  
 <223> Japanese encephalitis virus strain L48967 region  
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 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain L48968 region  
       of conserved sequence in 3' untranslated region  
  
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99  
  
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 <223> Japanese encephalitis virus strain AY184212 region  
       of conserved sequence in 3' untranslated region  
  
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 cgtctcggaa gaaggtccct gtcactgga tgttgggaag 99  
  
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 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AY251616 region  
       of conserved sequence in 3' untranslated region  
  
 <400> 205  
 cagtcccagg aggactgggt taacaaatct gacaacggaa ggtgggaaag ccctcagaac 60  
 cgtctcggaa gtaggtccct gtcaccgga agttgaaag 99  
  
 <210> 206  
 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AY278556 region  
       of conserved sequence in 3' untranslated region



<400> 206  
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 cgtctcggaa gcaggtccct gtcaccgga agttgaaag 99

<210> 207  
 <211> 99  
 <212> DNA  
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<220>  
 <223> Japanese encephalitis virus strain AY316157 region  
 of conserved sequence in 3' untranslated region

<400> 207  
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<210> 208  
 <211> 99  
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<220>  
 <223> Japanese encephalitis virus strain L54067 region  
 of conserved sequence in 3' untranslated region

<400> 208  
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 209  
 <211> 99  
 <212> DNA  
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<220>  
 <223> Japanese encephalitis virus strain L54068 region  
 of conserved sequence in 3' untranslated region

<400> 209  
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 210  
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<220>  
 <223> Japanese encephalitis virus strain L54069 region  
 of conserved sequence in 3' untranslated region

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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 211  
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<220>  
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 of conserved sequence in 3' untranslated region

<400> 211  
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

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 <212> DNA  
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<220>  
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 of conserved sequence in 3' untranslated region

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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 213  
 <211> 99  
 <212> DNA  
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<220>  
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 of conserved sequence in 3' untranslated region

<400> 213  
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 214  
 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain L54122 region  
 of conserved sequence in 3' untranslated region

<400> 214  
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 215  
 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain L54123 region  
 of conserved sequence in 3' untranslated region

<400> 215  
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 216  
 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF306514 region  
       of conserved sequence in 3' untranslated region  
  
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 cgtctcggaa gctctccct tctcaccgga agttgaaag 99  
  
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 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF306515 region  
       of conserved sequence in 3' untranslated region  
  
 <400> 217  
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 cgtttcggaa gtaggtccct tctcactgga agttgaaag 99  
  
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 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF306516 region  
       of conserved sequence in 3' untranslated region  
  
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 cgtttcggaa gtaggtccct tctcactgga agttgaaag 99  
  
 <210> 219  
 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF306517 region  
       of conserved sequence in 3' untranslated region  
  
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 cgtttcggaa gtaggtccct tctcactgga agttgaaag 99  
  
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 <211> 97  
 <212> DNA  
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 <223> St. Louis encephalitis virus strain BFS1750-C  
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<400> 220  
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<210> 221  
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 <212> DNA  
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<220>  
 <223> St. Louis encephalitis virus strain 1750-Std  
 region of conserved sequence in 3' untranslated  
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<400> 221  
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 actcgggagg gtccctagca cgtaggctgg agaggac 97

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 <212> DNA  
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<220>  
 <223> St. Louis encephalitis virus strain TD6-4G-C  
 region of conserved sequence in 3' untranslated  
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<400> 222  
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 actcgggagg gtccctggca cgtaggctgg agaggac 97

<210> 223  
 <211> 97  
 <212> DNA  
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<220>  
 <223> St. Louis encephalitis virus strain TD6-4G-20  
 region of conserved sequence in 3' untranslated  
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<400> 223  
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 actcgggagg gtccctggca cgtaggctgg agaggac 97

<210> 224  
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 <212> DNA  
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<220>  
 <223> St. Louis encephalitis virus strain CoaV750  
 region of conserved sequence in 3' untranslated  
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<400> 224  
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 attcgggagg gtccctggca cgtaggctgg agaggac 97

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 <212> DNA  
 <213> St. Louis encephalitis virus  
  
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 <223> St. Louis encephalitis virus strain L695121.05  
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 actcgggagg gtccctggca ttaggctgg agaggac 97  
  
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 <220>  
 <223> St. Louis encephalitis virus strain TNM771K-C  
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       region  
  
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 actcgggagg gtccctggca ctaggctgg agaggac 97  
  
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 <220>  
 <223> St. Louis encephalitis virus strain MSI-7-C  
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       region  
  
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 actcgggagg gtccctggca ctaggctgg agaggac 97  
  
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 <213> St. Louis encephalitis virus  
  
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 <223> St. Louis encephalitis virus strain Kern217  
       region of conserved sequence in 3' untranslated  
       region  
  
 <400> 228  
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 actcgggagg gtccctggca ctaggctgg agaggac 97  
  
 <210> 229  
 <211> 93  
 <212> DNA  
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<220>  
 <223> St. Louis encephalitis virus strain CoaV608  
 region of conserved sequence in 3' untranslated  
 region

<400> 229  
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 gggaggggtcc ctggcacgta ggctggagag gac 93

<210> 230  
 <211> 97  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain TBH-28  
 region of conserved sequence in 3' untranslated  
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<400> 230  
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 actcgggagg gtccctggca cgtaggcccg agaggac 97

<210> 231  
 <211> 97  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain VR1265  
 region of conserved sequence in 3' untranslated  
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<400> 231  
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 actcgggagg gtccctggca cgtaggctgg agcggac 97

<210> 232  
 <211> 93  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain CoaV353  
 region of conserved sequence in 3' untranslated  
 region

<400> 232  
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 gggaggggtcc ctggcacgta ggctggagag gac 93

<210> 233  
 <211> 100  
 <212> DNA  
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<220>  
 <223> Murray Valley encephalitis virus strain VR77  
 region of conserved sequence in 3' untranslated  
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<400> 233  
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 ccgtctcgga agaggagtcc ctgccaacaa tggagatgaa 100

<210> 234  
 <211> 100  
 <212> DNA  
 <213> Murray Valley encephalitis virus

<220>  
 <223> Murray Valley encephalitis virus strain AF161266  
 region of conserved sequence in 3' untranslated  
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<400> 234  
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 ccgtctcgga agaggagtcc ctgccaacaa tggagatgaa 100

<210> 235  
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 <212> DNA  
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<220>  
 <223> Murray Valley encephalitis virus strain M35172  
 region of conserved sequence in 3' untranslated  
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<400> 235  
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 ccgtctcgga agaggagtcc ctgccaacaa tggagatgaa 100

<210> 236  
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 <212> DNA  
 <213> Murray Valley encephalitis virus

<220>  
 <223> Murray Valley encephalitis virus strain L48972  
 region of conserved sequence in 3' untranslated  
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<400> 236  
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 ccgtctcgga agaggagtcc ctccaacaa tggagatgaa 100

<210> 237  
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 <212> DNA  
 <213> Murray Valley encephalitis virus

<220>  
 <223> Murray Valley encephalitis virus strain L48973  
 region of conserved sequence in 3' untranslated  
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<400> 237  
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 ccgtctcgga agaggagtcc ctgccaacaa tggagatgaa 100

<210> 238  
 <211> 100  
 <212> DNA  
 <213> Murray Valley encephalitis virus  
  
 <220>  
 <223> Murray Valley encephalitis virus strain L48974  
       region of conserved sequence in 3' untranslated  
       region  
  
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 ccgtctcgga agaggagccc ctgccaacaa tggagatgaa 100  
  
 <210> 239  
 <211> 100  
 <212> DNA  
 <213> Murray Valley encephalitis virus  
  
 <220>  
 <223> Murray Valley encephalitis virus strain L48975  
       region of conserved sequence in 3' untranslated  
       region  
  
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 ccgtctcgga agaggagtcc cttccaacaa tggagatgaa 100  
  
 <210> 240  
 <211> 100  
 <212> DNA  
 <213> Murray Valley encephalitis virus  
  
 <220>  
 <223> Murray Valley encephalitis virus strain L48976  
       region of conserved sequence in 3' untranslated  
       region  
  
 <400> 240  
 caaccccagg aggactgggt taccaaagct gattctccac gggtggaaag cctcccagaa 60  
 ccgtttcgga agaggagtcc ctgctaacaa tggagatgaa 100  
  
 <210> 241  
 <211> 98  
 <212> DNA  
 <213> Koutango virus  
  
 <220>  
 <223> Koutango virus strain L48980 region of conserved  
       sequence in 3' untranslated region  
  
 <400> 241  
 caaccccagg aggactgggt caacaaatct gcgaggagat ccacgtaatc cctcagaacc 60  
 gtctcggaag gaggacccca cgtgttttat tctcaaag 98  
  
 <210> 242  
 <211> 105  
 <212> DNA  
 <213> West Nile virus



<220>  
 <223> West Nile virus strain AF260967 region of  
 conserved sequence in 3' untranslated region

<400> 242  
 tggctgaagc tgtaggctcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 243  
 <211> 105  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF260968 region of  
 conserved sequence in 3' untranslated region

<400> 243  
 tgactgaagc tgtaggctcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 244  
 <211> 105  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF260969 region of  
 conserved sequence in 3' untranslated region

<400> 244  
 tggctgaagc tgtaggctcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 245  
 <211> 105  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF481864 region of  
 conserved sequence in 3' untranslated region

<400> 245  
 tgactgaagc tgtaggctcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 246  
 <211> 103  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain M12294 region of  
 conserved sequence in 3' untranslated region

<400> 246  
 tggctgaagc tgtaagccaa gggaaggact agaggttaga ggagaccccg tgccaaaaaac 60  
 accaaaaagaa acagcatatt gacacctggg atagactagg gga 103

<210> 247  
 <211> 105  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF206518 region of  
       conserved sequence in 3' untranslated region  
  
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 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105  
  
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 <211> 105  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF317203 region of  
       conserved sequence in 3' untranslated region  
  
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 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105  
  
 <210> 249  
 <211> 105  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF202541 region of  
       conserved sequence in 3' untranslated region  
  
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 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105  
  
 <210> 250  
 <211> 105  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF404757 region of  
       conserved sequence in 3' untranslated region  
  
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 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105  
  
 <210> 251  
 <211> 105  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF404753 region of  
       conserved sequence in 3' untranslated region

<400> 251  
 tggctgaagc tgtagggtcag gggaaggact agagggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 252  
 <211> 105  
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<220>  
 <223> West Nile virus strain AF404754 region of  
 conserved sequence in 3' untranslated region

<400> 252  
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 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 253  
 <211> 105  
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<220>  
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 conserved sequence in 3' untranslated region

<400> 253  
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 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 254  
 <211> 105  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF404756 region of  
 conserved sequence in 3' untranslated region

<400> 254  
 tggctgaagc tgtagggtcag gggaaggact agagggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 255  
 <211> 105  
 <212> DNA  
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<220>  
 <223> West Nile virus strain AF017254 region of  
 conserved sequence in 3' untranslated region

<400> 255  
 tgactgaagc tgtagggtcag gggaaggact agagggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgataacctg ggatagacta ggaga 105

<210> 256  
 <211> 105  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF533540 region of  
 conserved sequence in 3' untranslated region

<400> 256  
 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 257  
 <211> 105  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AY262283 region of  
 conserved sequence in 3' untranslated region

<400> 257  
 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccgcaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 258  
 <211> 105  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AY278441 region of  
 conserved sequence in 3' untranslated region

<400> 258  
 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 259  
 <211> 105  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AY268132 region of  
 conserved sequence in 3' untranslated region

<400> 259  
 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 260  
 <211> 105  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AY268133 region of  
 conserved sequence in 3' untranslated region

<400> 260  
 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 261  
 <211> 105  
 <212> DNA  
 <213> Kunjin virus  
  
 <220>  
 <223> Kunjin virus strain AY274504 region of conserved  
           sequence in 3' untranslated region  
  
 <400> 261  
 tggctgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccgcaaaa 60  
 caccacaaca acacagcata ttgacacctg ggatagacta ggaga 105  
  
 <210> 262  
 <211> 105  
 <212> DNA  
 <213> Kunjin virus  
  
 <220>  
 <223> Kunjin virus strain AY274505 region of conserved  
           sequence in 3' untranslated region  
  
 <400> 262  
 tggctgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccgcaaaa 60  
 caccacaaca acacagcata ttgacacctg ggatagacta ggaga 105  
  
 <210> 263  
 <211> 105  
 <212> DNA  
 <213> Kunjin virus  
  
 <220>  
 <223> Kunjin virus strain L24512 region of conserved  
           sequence in 3' untranslated region  
  
 <400> 263  
 tggctgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccgcaaaa 60  
 caccacaaca acacagcata ttgacacctg ggatagacta ggaga 105  
  
 <210> 264  
 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AB051292 region  
           of conserved sequence in 3' untranslated region  
  
 <400> 264  
 cccctcgaag ctgtggagga ggtggaagga ctagaggta gaggagacc cgcatttgca 60  
 tcaaaacagc atattgacac ctgggaatag actgggaga 99  
  
 <210> 265  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF014160 region  
           of conserved sequence in 3' untranslated region

<400> 265  
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 266  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF014161 region  
 of conserved sequence in 3' untranslated region

<400> 266  
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 267  
 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF045551 region  
 of conserved sequence in 3' untranslated region

<400> 267  
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 atcaaacagc atattgacac ctgggaatag agtgggaga 99

<210> 268  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF069076 region  
 of conserved sequence in 3' untranslated region

<400> 268  
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 269  
 <211> 98  
 <212> DNA  
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<220>  
 <223> Japanese encephalitis virus strain AF075723 region  
 of conserved sequence in 3' untranslated region

<400> 269  
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 270  
 <211> 98  
 <212> DNA  
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<220>  
 <223> Japanese encephalitis virus strain AF080251 region  
 of conserved sequence in 3' untranslated region

<400> 270  
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 271  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF098735 region  
 of conserved sequence in 3' untranslated region

<400> 271  
 ctccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 272  
 <211> 98  
 <212> DNA  
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<220>  
 <223> Japanese encephalitis virus strain AF098736 region  
 of conserved sequence in 3' untranslated region

<400> 272  
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 273  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF098737 region  
 of conserved sequence in 3' untranslated region

<400> 273  
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 tcaaacagca tattgacacc tgggataga ctgggaga 98

<210> 274  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF217620 region  
 of conserved sequence in 3' untranslated region

<400> 274  
 ttccctcgaag ctgtagagga agtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 275  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF221499 region  
       of conserved sequence in 3' untranslated region  
  
 <400> 275  
 ctctctgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98  
  
 <210> 276  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF221500 region  
       of conserved sequence in 3' untranslated region  
  
 <400> 276  
 ctctctgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98  
  
 <210> 277  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF254452 region  
       of conserved sequence in 3' untranslated region  
  
 <400> 277  
 ccctctgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98  
  
 <210> 278  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF254453 region  
       of conserved sequence in 3' untranslated region  
  
 <400> 278  
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98  
  
 <210> 279  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF315119 region  
       of conserved sequence in 3' untranslated region



<400> 279  
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 280  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF416457 region  
 of conserved sequence in 3' untranslated region

<400> 280  
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 281  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF486638 region  
 of conserved sequence in 3' untranslated region

<400> 281  
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 tcaaacagca tattgacacc tgggaatata ctgggaga 98

<210> 282  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain U14163 region  
 of conserved sequence in 3' untranslated region

<400> 282  
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 283  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain U15763 region  
 of conserved sequence in 3' untranslated region

<400> 283  
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 284  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain L48961 region  
 of conserved sequence in 3' untranslated region

<400> 284  
 ctccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 285  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain U47032 region  
 of conserved sequence in 3' untranslated region

<400> 285  
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 tcaaacagca tattgacacc tgggaataga ctaggaga 98

<210> 286  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain M18370 region  
 of conserved sequence in 3' untranslated region

<400> 286  
 ccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 287  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain M55506 region  
 of conserved sequence in 3' untranslated region

<400> 287  
 ccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 288  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain L78128 region  
 of conserved sequence in 3' untranslated region

<400> 288  
 ccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 289  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain D90195 region  
         of conserved sequence in 3' untranslated region  
  
 <400> 289  
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98  
  
 <210> 290  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain D90194 region  
         of conserved sequence in 3' untranslated region  
  
 <400> 290  
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98  
  
 <210> 291  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF311748 region  
         of conserved sequence in 3' untranslated region  
  
 <400> 291  
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98  
  
 <210> 292  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AY184212 region  
         of conserved sequence in 3' untranslated region  
  
 <400> 292  
 cccttcgaag ctgtagaaga ggtggaagga ctagagggtta gaggagaccc cgcattctgca 60  
 tcaaacagca tattgacacc tgggaataga ctaggaga 98  
  
 <210> 293  
 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AY316157 region  
         of conserved sequence in 3' untranslated region

<400> 293  
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcaatttgc 60  
 atcaaacagc atattgacac ctgggaatag actgggaga 99

<210> 294  
 <211> 99  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF306514 region  
 of conserved sequence in 3' untranslated region

<400> 294  
 cccctcgaag ctgtagagga ggtgtaagga atagagggtta gaggagaccc cgcaatttgc 60  
 atcaaacagc atattgacac ctgggaatag agtgggaga 99

<210> 295  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF306515 region  
 of conserved sequence in 3' untranslated region

<400> 295  
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 296  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF306516 region  
 of conserved sequence in 3' untranslated region

<400> 296  
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 297  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF306517 region  
 of conserved sequence in 3' untranslated region

<400> 297  
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 tcaaacagca tattgacacc tgggaataga gtgggaga 98

<210> 298  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain D00037 region  
 of conserved sequence in 3' untranslated region

<400> 298  
 cctcttgtag cttttgaggt ggttgaaggt cttgaggttt gaggagtccc cgtctttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 299  
 <211> 98  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain M14933 region  
 of conserved sequence in 3' untranslated region

<400> 299  
 cctcttgtag cttttgaggt ggttgaaggt cttgaggttt gaggagtccc cgtctttgca 60  
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 300  
 <211> 100  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain BFS1750-C  
 region of conserved sequence in 3' untranslated  
 region

<400> 300  
 ccgctcgaag ctgtagagac gggggaagga ctagaggta gaggagaccc cttgccgtta 60  
 acgcaaaca cagcatattg acacctggaa agacaggaga 100

<210> 301  
 <211> 27  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain 1750-Std  
 region of conserved sequence in 3' untranslated  
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<400> 301  
 ccgctcgaag ctgtagagac gggggaa 27

<210> 302  
 <211> 100  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain TD6-4G-C  
 region of conserved sequence in 3' untranslated  
 region

<400> 302  
 ccgctcgaag ctgtagagat gggggaagga ctagaggta gaggagaccc cttgccgtta 60  
 acgcaaaca cagcatattg acacctggaa agacaggaga 100

<210> 303  
 <211> 100  
 <212> DNA  
 <213> St. Louis encephalitis virus  
  
 <220>  
 <223> St. Louis encephalitis virus strain TD6-4G-20  
       region of conserved sequence in 3' untranslated  
       region  
  
 <400> 303  
 ccgctcgaag ctgtagagat gggggaagga ctagagggtta gaggagaccc cttgccgtta 60  
 acgcaaacia cagcatattg acacctggaa agacaggaga 100  
  
 <210> 304  
 <211> 27  
 <212> DNA  
 <213> St. Louis encephalitis virus  
  
 <220>  
 <223> St. Louis encephalitis virus strain CoaV750  
       region of conserved sequence in 3' untranslated  
       region  
  
 <400> 304  
 ccgctcgaag ctgtagagat gggggaa 27  
  
 <210> 305  
 <211> 100  
 <212> DNA  
 <213> St. Louis encephalitis virus  
  
 <220>  
 <223> St. Louis encephalitis virus strain L695121.05  
       region of conserved sequence in 3' untranslated  
       region  
  
 <400> 305  
 ccgctcgaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60  
 acgcaaacia cagcatattg acacctggaa agacaggaga 100  
  
 <210> 306  
 <211> 100  
 <212> DNA  
 <213> St. Louis encephalitis virus  
  
 <220>  
 <223> St. Louis encephalitis virus strain TNM771K-C  
       region of conserved sequence in 3' untranslated  
       region  
  
 <220>  
 <221> modified\_base  
 <222> (68)...(68)  
 <223> n = g, a, c or t  
  
 <400> 306  
 ccgctcgaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60  
 acgcaaanaa cagcatattg acacctggaa agacaggaga 100

<210> 307  
 <211> 100  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain MSI-7-C  
 region of conserved sequence in 3' untranslated  
 region

<400> 307  
 ccgctcaaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60  
 acgcaaacaa cagcatattg acacctggaa agacaggaga 100

<210> 308  
 <211> 95  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain Kern217  
 region of conserved sequence in 3' untranslated  
 region

<400> 308  
 ccgctcaaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60  
 acgcaaacaa cagcatattg acacctggaa agaca 95

<210> 309  
 <211> 100  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain CoaV608  
 region of conserved sequence in 3' untranslated  
 region

<400> 309  
 ccgctcaaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60  
 acgcaaacaa cagcatattg acacctggaa agacaggaga 100

<210> 310  
 <211> 95  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain TBH-28  
 region of conserved sequence in 3' untranslated  
 region

<400> 310  
 ccgctcgaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60  
 acgcaaacaa cagcatattg acacctggaa agaca 95

<210> 311  
 <211> 92  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain VR1265  
 region of conserved sequence in 3' untranslated  
 region

<400> 311  
 ccgctcgaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtca 60  
 acgcaaacaa cagcatattg acacctggaa ag 92

<210> 312  
 <211> 100  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain CoaV353  
 region of conserved sequence in 3' untranslated  
 region

<400> 312  
 ccgctcgaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60  
 acgcaaacaa cagcatattg acacctggaa agacaggaga 100

<210> 313  
 <211> 104  
 <212> DNA  
 <213> Murray Valley encephalitis virus

<220>  
 <223> Murray Valley encephalitis virus strain VR77  
 region of conserved sequence in 3' untranslated  
 region

<400> 313  
 tcgccgaagc tgtaaggcgg gtggacggac tagagggttag aggagacccc actctcaaaa 60  
 gcatcaaaca acagcatatt gacacctggg aaaagactag gaga 104

<210> 314  
 <211> 104  
 <212> DNA  
 <213> Murray Valley encephalitis virus

<220>  
 <223> Murray Valley encephalitis virus strain AF161266  
 region of conserved sequence in 3' untranslated  
 region

<400> 314  
 tcgccgaagc tgtaaggcgg gtggacggac tagagggttag aggagacccc actctcaaaa 60  
 gcatcaaaca acagcatatt gacacctggg aaaagactag gaga 104

<210> 315  
 <211> 100  
 <212> DNA  
 <213> Murray Valley encephalitis virus

<220>  
 <223> Murray Valley encephalitis virus strain M35172  
 region of conserved sequence in 3' untranslated  
 region



<400> 315  
 tcgccgaagc tgtaaggcgg gtggacggac tagaggtttag aggagacccc actctcaaaa 60  
 gcatcaaaaca acagcatatt gacacctggg aaaagactag 100

<210> 316  
 <211> 121  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF260967 region of  
 conserved sequence in 3' untranslated region

<400> 316  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60  
 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120  
 a 121

<210> 317  
 <211> 121  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF260968 region of  
 conserved sequence in 3' untranslated region

<400> 317  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60  
 gactgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120  
 a 121

<210> 318  
 <211> 121  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF260969 region of  
 conserved sequence in 3' untranslated region

<400> 318  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt tgaagtgcac ggcccagcct 60  
 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120  
 a 121

<210> 319  
 <211> 121  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF481864 region of  
 conserved sequence in 3' untranslated region

<400> 319  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60  
 gactgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120  
 a 121

<210> 320  
 <211> 120  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain M12294 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 320  
 cagggagaag ggactagagg ttagaggaga cccgcgctaa aaaagtgcac ggcccaactt 60  
 ggctgaagct gtaagccaag ggaaggacta gaggttagag gagaccccgt gccaaaaaca 120  
  
 <210> 321  
 <211> 121  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF206518 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 321  
 cagggcgaaa ggactagagg ttagaggaga cccgcggtt taaagtgcac ggcccagcct 60  
 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120  
 a 121  
  
 <210> 322  
 <211> 121  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF317203 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 322  
 cagggcgaaa ggactagagg ttagaggaga cccgcggtt tgaagtgcac ggcccagcct 60  
 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120  
 a 121  
  
 <210> 323  
 <211> 121  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AF202541 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 323  
 cagggcgaaa ggactagagg ttagaggaga cccgcggtt taaagtgcac ggcccagcct 60  
 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120  
 a 121  
  
 <210> 324  
 <211> 121  
 <212> DNA  
 <213> West Nile virus

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<220>
<223> West Nile virus strain AF404757 region of
      conserved sequence in 3' untranslated region

<400> 324
cagggcgaaa ggactagagg ttagaggaga ccccgcggtt tgaagagcac ggcccagcct 60
ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
a                                                    121

<210> 325
<211> 121
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404753 region of
      conserved sequence in 3' untranslated region

<400> 325
cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60
ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
a                                                    121

<210> 326
<211> 121
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404754 region of
      conserved sequence in 3' untranslated region

<400> 326
cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60
ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
a                                                    121

<210> 327
<211> 121
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404755 region of
      conserved sequence in 3' untranslated region

<400> 327
cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60
ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
a                                                    121

<210> 328
<211> 121
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404756 region of
      conserved sequence in 3' untranslated region

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<400> 328  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60  
 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120  
 a 121

<210> 329  
 <211> 121  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF017254 region of  
 conserved sequence in 3' untranslated region

<400> 329  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60  
 gactgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120  
 a 121

<210> 330  
 <211> 87  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF208017 region of  
 conserved sequence in 3' untranslated region

<400> 330  
 cagggagaag ggactagtgg ttagaggaga ccccacgtta aaaagtgcac ggcccaactt 60  
 ggctgaagct gtaagccaag ggaagga 87

<210> 331  
 <211> 121  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF533540 region of  
 conserved sequence in 3' untranslated region

<400> 331  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60  
 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120  
 a 121

<210> 332  
 <211> 121  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AY262283 region of  
 conserved sequence in 3' untranslated region

<400> 332  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt tgaagtgcac ggcccagcct 60  
 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccgcaaaaac 120  
 a 121

<210> 333  
 <211> 95  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AY277251 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 333  
 caaggagaag ggactagagg ttagcggaga ccctgcgcat atagaaagag aggcacggcc 60  
 cagcctgaca gaagctgtaa gtcaggggaa ggact 95  
  
 <210> 334  
 <211> 118  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AY277252 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 334  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt tgaagtgcac ggcccatggc 60  
 tgaagctgta ggtcagggga aggactagag gttagtggag acccgtgcc aaaaaaca 118  
  
 <210> 335  
 <211> 59  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AY278441 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 335  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt tgaagtgcac ggcccagcc 59  
  
 <210> 336  
 <211> 115  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AY278442 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 336  
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt tgaagtgcac ggctggctga 60  
 agctgtaggt caggggaagg actagagggt agtggagacc ccgtgccaca aaaca 115  
  
 <210> 337  
 <211> 121  
 <212> DNA  
 <213> West Nile virus  
  
 <220>  
 <223> West Nile virus strain AY268132 region of  
       conserved sequence in 3' untranslated region

<400> 337  
 cagggcgaaa ggactagagg ttagaggaga cccgcggtt tgaagtgcac ggcccagcct 60  
 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccggt gccacaaaac 120  
 a 121

<210> 338  
 <211> 121  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AY268133 region of conserved sequence in 3' untranslated region

<400> 338  
 cagggcgaaa ggactagagg ttagaggaga cccgcggtt taaagtgcac ggcccagcct 60  
 gactgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccggt gccacagaaac 120  
 a 121

<210> 339  
 <211> 59  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AY490240 region of conserved sequence in 3' untranslated region

<400> 339  
 cagggcgaaa ggactagagg ttagaggaga cccgcggtt taaagtgcac ggcccagcc 59

<210> 340  
 <211> 121  
 <212> DNA  
 <213> Kunjin virus

<220>  
 <223> Kunjin virus strain AY274504 region of conserved sequence in 3' untranslated region

<400> 340  
 cagagtgaata ggactagagg ttagaggaga cccgcggtt tgaagtgcac ggcccagcct 60  
 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccggt gccgcaaaaac 120  
 a 121

<210> 341  
 <211> 121  
 <212> DNA  
 <213> Kunjin virus

<220>  
 <223> Kunjin virus strain AY274505 region of conserved sequence in 3' untranslated region

<400> 341  
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 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccggt gccgcaaaaac 120  
 a 121

<210> 342  
 <211> 121  
 <212> DNA  
 <213> Kunjin virus  
  
 <220>  
 <223> Kunjin virus strain L24512 region of conserved  
           sequence in 3' untranslated region  
  
 <400> 342  
 cagagtgaaa ggactagagg ttagaggaga cccgcggttc tgaagtgcac ggcccagcct 60  
 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccgcaaaac 120  
 a 121  
  
 <210> 343  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AB051292 region  
           of conserved sequence in 3' untranslated region  
  
 <400> 343  
 ctaggtgtaa ggactagagg ttagaggaga ccccggtgaa acaacattat gcggcccaag 60  
 cccctcgaa gctgtgagg aggtggaagg actagaggtt agaggagacc ccgcatttgc 120  
 atcaa 125  
  
 <210> 344  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF014160 region  
           of conserved sequence in 3' untranslated region  
  
 <400> 344  
 cgaggtgtaa ggactagagg ttagaggaga ccccggtgaa acaacaacat gcggcccaag 60  
 cccctcgaa gctgtagagg aggtggaagg actagaggtt agaggagacc ccgcatttgc 120  
 atcaa 125  
  
 <210> 345  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF014161 region  
           of conserved sequence in 3' untranslated region  
  
 <400> 345  
 cgaggtgtaa ggactagagg ttagaggaga ccccggtgaa acaacaacat gcggcccaag 60  
 cccctcgaa gctgtagagg aggtggaagg actagaggtt agaggagacc ccgcatttgc 120  
 atcaa 125  
  
 <210> 346  
 <211> 125  
 <212> DNA  
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<220>  
 <223> Japanese encephalitis virus strain AF045551 region  
 of conserved sequence in 3' untranslated region

<400> 346  
 ttaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaaaattat gcggcccaag 60  
 cccctcgaa gctgtagagg aggtgtaagg aatagagggtt agaggagacc ccgcaatttg 120  
 catca 125

<210> 347  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF069076 region  
 of conserved sequence in 3' untranslated region

<400> 347  
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaacaacat gcggcccaag 60  
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 atcaa 125

<210> 348  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF075723 region  
 of conserved sequence in 3' untranslated region

<400> 348  
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa ataacaacat gcggcccaag 60  
 cccctcgaa gctgtagagg aggtggaagg actagagggtt agaggagacc ccgcatttgc 120  
 atcaa 125

<210> 349  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF080251 region  
 of conserved sequence in 3' untranslated region

<400> 349  
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaacaacat gcggcccaag 60  
 cccctcgaa gctgtagagg aggtggaagg actagagggtt agaggagacc ccgcatttgc 120  
 atcaa 125

<210> 350  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF098735 region  
 of conserved sequence in 3' untranslated region



<400> 350  
 cgaggtgtaa ggactagagg ttagaggaga ccccggtggaa acaacaacat gcggcccaag 60  
 cctcctcgaa gctgtagagg aggtggaagg actagagggtt agaggagacc ccgcatttgc 120  
 atcaa 125

<210> 351  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF098736 region  
 of conserved sequence in 3' untranslated region

<400> 351  
 cgaggtgtaa ggactagagg ttagaggaga ccccggtggaa acaacaacat gcggcccaag 60  
 cccctcga gctgtagagg aggtggaagg actagagggtt agaggagacc ccgcatttgc 120  
 atcaa 125

<210> 352  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF098737 region  
 of conserved sequence in 3' untranslated region

<400> 352  
 cgaggtgtaa ggactagagg ttagaggaga ccccggtggaa acaacaacat gcggcccaag 60  
 cccctcga gctgtagagg aggtggaagg actagagggtt agaggagacc ccgcatttgc 120  
 atcaa 125

<210> 353  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF217620 region  
 of conserved sequence in 3' untranslated region

<400> 353  
 cgaggtgtaa ggactagagg ttagaggaga ccccggtggaa acaacaatat gcggcccaag 60  
 cttcctcgaa gctgtagagg aagtggaagg actagagggtt agaggagacc ccgcatttgc 120  
 atcaa 125

<210> 354  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain AF221499 region  
 of conserved sequence in 3' untranslated region

<400> 354  
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 cctcctcgaa gctgtagagg aggtggaagg actagagggtt agaggagacc ccgcatttgc 120  
 atcaa 125

<210> 355  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF221500 region  
       of conserved sequence in 3' untranslated region  
  
 <400> 355  
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaataacat gcggcccaag 60  
 cctcctcgaa gctgtagagg aggtggaagg actagagggt agaggagacc ccgcatttgc 120  
 atcaa 125  
  
 <210> 356  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF254452 region  
       of conserved sequence in 3' untranslated region  
  
 <400> 356  
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaacaacat gcggcccaag 60  
 cccctcgaa gctgtagagg aggtggaagg actagagggt agaggagacc ccgcatttgc 120  
 atcaa 125  
  
 <210> 357  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF254453 region  
       of conserved sequence in 3' untranslated region  
  
 <400> 357  
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaacaacat gcggcccaag 60  
 cccctcgaa gctgtagagg aggtggaagg actagagggt agaggagacc ccgcatttgc 120  
 atcaa 125  
  
 <210> 358  
 <211> 125  
 <212> DNA  
 <213> Japanese encephalitis virus  
  
 <220>  
 <223> Japanese encephalitis virus strain AF315119 region  
       of conserved sequence in 3' untranslated region  
  
 <400> 358  
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 atcaa 125  
  
 <210> 359  
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<220>  
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 atcaa 125

<210> 360  
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<220>  
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 of conserved sequence in 3' untranslated region

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 atcaa 125

<210> 361  
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<220>  
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 atcaa 125

<210> 362  
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<220>  
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 of conserved sequence in 3' untranslated region

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 atcaa 125

<210> 363  
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<220>  
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 of conserved sequence in 3' untranslated region

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 atcaa 125

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<220>  
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 atcaa 125

<210> 365  
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<220>  
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 of conserved sequence in 3' untranslated region

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 atcaa 125

<210> 366  
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<220>  
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 of conserved sequence in 3' untranslated region

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 atcaa 125

<210> 367  
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 atcaa 125

<210> 368  
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 atcaa 125  
  
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 atcaa 125  
  
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 ccccttcgaa gctgtagaag aggtggaagg actagagggtt agaggagacc ccgcatttgc 120  
 atcaa 125  
  
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<220>  
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<400> 372  
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 catca 125

<210> 373  
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 <212> DNA  
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<220>  
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 of conserved sequence in 3' untranslated region

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 cccctcgaa gctgtagagg aggtgtaagg aatagagggtt agaggagacc ccgcaatttg 120  
 catca 125

<210> 374  
 <211> 125  
 <212> DNA  
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<220>  
 <223> Japanese encephalitis virus strain AF306515 region  
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<400> 374  
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 atcaa 125

<210> 375  
 <211> 125  
 <212> DNA  
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<220>  
 <223> Japanese encephalitis virus strain AF306516 region  
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 atcaa 125

<210> 376  
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<220>  
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 of conserved sequence in 3' untranslated region

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 atcaa 125

<210> 377  
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<220>  
 <223> St. Louis encephalitis virus strain BFS1750 region  
 of conserved sequence in 3' untranslated region

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 gc 122

<210> 378  
 <211> 85  
 <212> DNA  
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<220>  
 <223> St. Louis encephalitis virus strain 1750-Std region  
 of conserved sequence in 3' untranslated region

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<210> 379  
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 <212> DNA  
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<220>  
 <223> St. Louis encephalitis virus strain TD6-4G region  
 of conserved sequence in 3' untranslated region

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 gc 122

<210> 380  
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 <212> DNA  
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<220>  
 <223> St. Louis encephalitis virus strain CoaV750 region  
 of conserved sequence in 3' untranslated region

<400> 380  
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 gctcgaagct gtagagatgg gggaa 85

<210> 381  
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 <223> St. Louis encephalitis virus strain L695121.05 region  
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 gc 122  
  
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 <223> St. Louis encephalitis virus strain TNM771K region  
       of conserved sequence in 3' untranslated region  
  
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 gc 122  
  
 <210> 383  
 <211> 122  
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 <220>  
 <223> St. Louis encephalitis virus strain MSI-7 region  
       of conserved sequence in 3' untranslated region  
  
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 gc 122  
  
 <210> 384  
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 <223> St. Louis encephalitis virus strain Kern217 region  
       of conserved sequence in 3' untranslated region  
  
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 catggcgtaa ggactagagg ttagaggaga ccccgctgta acttggcaag gcccaaacc 60  
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 gc 122  
  
 <210> 385  
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<220>  
 <223> St. Louis encephalitis virus strain CoaV608 region  
 of conserved sequence in 3' untranslated region

<400> 385  
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 gc 122

<210> 386  
 <211> 122  
 <212> DNA  
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<220>  
 <223> St. Louis encephalitis virus strain TBH-28 region  
 of conserved sequence in 3' untranslated region

<400> 386  
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 gc 122

<210> 387  
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 <212> DNA  
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<220>  
 <223> St. Louis encephalitis virus strain VR1265 region  
 of conserved sequence in 3' untranslated region

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 gc 122

<210> 388  
 <211> 122  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain CoaV353 region  
 of conserved sequence in 3' untranslated region

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 gc 122

<210> 389  
 <211> 119  
 <212> DNA  
 <213> Murray Valley encephalitis virus

<220>  
 <223> Murray Valley encephalitis virus strain VR77  
 region of conserved sequence in 3' untranslated  
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<210> 390  
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 <212> DNA  
 <213> Murray Valley encephalitis virus

<220>  
 <223> Murray Valley encephalitis virus strain AF161266  
 region of conserved sequence in 3' untranslated  
 region

<400> 390  
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 ccgaagctgt aaggcgggtg gacggactag aggttagagg agaccccact ctcaaaagc 119

<210> 391  
 <211> 119  
 <212> DNA  
 <213> Murray Valley encephalitis virus

<220>  
 <223> Murray Valley encephalitis virus strain M35172  
 region of conserved sequence in 3' untranslated  
 region

<400> 391  
 cccggcgaag gactagaggt tagaggagac cctgcggaag aaatgagtgg cccaagctcg 60  
 ccgaagctgt aaggcgggtg gacggactag aggttagagg agaccccact ctcaaaagc 119

<210> 392  
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 <212> DNA  
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<220>  
 <223> Dengue virus type 1 strain U88537 region of  
 conserved sequence in 3' untranslated region

<400> 392  
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 gcacaacaac a 131

<210> 393  
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<220>  
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 conserved sequence in 3' untranslated region

<400> 393  
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 gcacaacaac a 131

<210> 394  
 <211> 131  
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 <220>  
 <223> Dengue virus type 1 strain U88535 region of  
       conserved sequence in 3' untranslated region  
  
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       conserved sequence in 3' untranslated region  
  
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 <210> 396  
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 <223> Dengue virus type 1 strain AY206457 region of  
       conserved sequence in 3' untranslated region  
  
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 gcacaacaac a 131  
  
 <210> 397  
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 <223> Dengue virus type 1 strain AY145123 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 397  
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 cccaagacta gaggttagag gagaccccc gcacaacaac a 101  
  
 <210> 398  
 <211> 131  
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<220>  
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 gcacaacaac a 131

<210> 399  
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 <213> Dengue virus type 1

<220>  
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 gcacaacaac a 131

<210> 400  
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<220>  
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 gcacaacaac a 131

<210> 401  
 <211> 131  
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<220>  
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 gcataacaac a 131

<210> 402  
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<220>  
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<400> 402  
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 gcataacaac a 131

<210> 403  
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 <212> DNA  
 <213> Dengue virus type 1

<220>  
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 conserved sequence in 3' untranslated region

<400> 403  
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 gcacaacaac a 131

<210> 404  
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<220>  
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 conserved sequence in 3' untranslated region

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 gcataacaac a 131

<210> 405  
 <211> 131  
 <212> DNA  
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<220>  
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 conserved sequence in 3' untranslated region

<400> 405  
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 cccaacacca ggggaagctg taccttgggtg gtaaggacta gaggttagag gagaccccc 120  
 gcacaacaac a 131

<210> 406  
 <211> 131  
 <212> DNA  
 <213> Dengue virus type 1

<220>  
 <223> Dengue virus type 1 strain AF350498 region of  
 conserved sequence in 3' untranslated region

<400> 406  
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 cccaacacca ggggaagctg taccctgggtg gtaaggacta gaggttagag gagaccccc 120  
 gcataacaat a 131

<210> 407  
 <211> 131  
 <212> DNA  
 <213> Dengue virus type 1  
  
 <220>  
 <223> Dengue virus type 1 strain AF311958 region of  
       conserved sequence in 3' untranslated region  
  
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 cccaacacca tgggaagctg taccttgggt gtaaggacta gaggttagag gagaccccc 120  
 gctcaacaac a 131  
  
 <210> 408  
 <211> 131  
 <212> DNA  
 <213> Dengue virus type 1  
  
 <220>  
 <223> Dengue virus type 1 strain AF311957 region of  
       conserved sequence in 3' untranslated region  
  
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 cccaacacca tgggaagctg taccttgggt gtaaggacta gaggttagag gagaccccc 120  
 gcacaacaac a 131  
  
 <210> 409  
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 <212> DNA  
 <213> Dengue virus type 1  
  
 <220>  
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       conserved sequence in 3' untranslated region  
  
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 cccaacacca tgggaagctg taccttgggt gtaaggacta gaggttagag gagaccccc 120  
 gcacaacaac a 131  
  
 <210> 410  
 <211> 97  
 <212> DNA  
 <213> Dengue virus type 1  
  
 <220>  
 <223> Dengue virus type 1 strain AF310148 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 410  
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 cccaacacca ggggaagctg taccctgggt gtaagga 97  
  
 <210> 411  
 <211> 131  
 <212> DNA  
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<220>  
 <223> Dengue virus type 1 strain AF310147 region of conserved sequence in 3' untranslated region

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 gcataacaat a 131

<210> 412  
 <211> 131  
 <212> DNA  
 <213> Dengue virus type 1

<220>  
 <223> Dengue virus type 1 strain AF310146 region of conserved sequence in 3' untranslated region

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 cccaacacca tgggaagctg taccttgggt gtaaggacta gaggttagag gagaccccc 120  
 gcacaacaac a 131

<210> 413  
 <211> 131  
 <212> DNA  
 <213> Dengue virus type 1

<220>  
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<220>  
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<210> 415  
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<220>  
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gcacaacaac a 131

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<220>  
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conserved sequence in 3' untranslated region

<400> 416  
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gcacaacaac a 131

<210> 417  
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conserved sequence in 3' untranslated region

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gcacaacaac a 131

<210> 418  
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conserved sequence in 3' untranslated region

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gcacaacaac a 131

<210> 419  
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<220>  
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conserved sequence in 3' untranslated region

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gcgtaacaat a 131



<210> 420  
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<210> 425  
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<220>  
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 ccccgaaaca aaa 133

<210> 426  
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 <212> DNA  
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<220>  
 <223> Dengue virus type 2 strain AF022436 region of conserved sequence in 3' untranslated region

<400> 426  
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 ccccgaaaca aaa 133

<210> 427  
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<220>  
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 ccccgaaaca aaa 133

<210> 428  
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<220>  
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<210> 429  
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<220>  
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<210> 430  
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<220>  
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 ccccgaaaca aaa 133

<210> 431  
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 ccccgaaaca aaa 133

<210> 432  
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 conserved sequence in 3' untranslated region

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<210> 433  
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 conserved sequence in 3' untranslated region

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<210> 434  
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<210> 435  
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 conserved sequence in 3' untranslated region

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<210> 436  
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 conserved sequence in 3' untranslated region

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<210> 437  
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<210> 438  
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<210> 439  
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<210> 440  
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<220>  
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<400> 440  
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 cccaagaca aaa 133

<210> 441  
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<220>  
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 ccccaaaaac aaaa 134

<210> 442  
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 <212> DNA  
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<220>  
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 conserved sequence in 3' untranslated region

<400> 442  
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 ccccgaaaca aaa 133

<210> 443  
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 conserved sequence in 3' untranslated region

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<210> 444  
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 conserved sequence in 3' untranslated region

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<210> 445  
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<210> 446  
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 conserved sequence in 3' untranslated region

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<210> 448  
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<220>  
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 conserved sequence in 3' untranslated region

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 cccaagaca aaa 133

<210> 449  
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 conserved sequence in 3' untranslated region

<400> 449  
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<210> 450  
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<220>  
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 cccccaaaaa caaa 134

<210> 451  
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 cccccaaaaa caaa 134

<210> 452  
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<210> 453  
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 cccccaaaca aaa 133

<210> 454  
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ccccgaaaca aaa 133

<210> 455
<211> 133
<212> DNA
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ccccgaaaca aaa 133

<210> 456
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<212> DNA
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<220>
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        conserved sequence in 3' untranslated region

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ccccgaaaca aaa 133

<210> 457
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
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        conserved sequence in 3' untranslated region

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ccccgaaaca aaa 133

<210> 458
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF169680 region of
        conserved sequence in 3' untranslated region

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ccccgaaaca aaa 133

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<210> 459  
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       conserved sequence in 3' untranslated region  
  
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 ccccgaaaca aaa 133  
  
 <210> 460  
 <211> 133  
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 <213> Dengue virus type 2  
  
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 ccccgaaaca aaa 133  
  
 <210> 461  
 <211> 133  
 <212> DNA  
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 ccccgaaaca aaa 133  
  
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       conserved sequence in 3' untranslated region  
  
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 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120  
 ccccgaaaca aaa 133  
  
 <210> 463  
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<220>
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gggcccgaagg cgagatgaag ctgtagtctc gctggaagga ctagagggtta gaggagaccc 120
ccccgaaaca aaa                                     133

<210> 464
<211> 133
<212> DNA
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<220>
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        conserved sequence in 3' untranslated region

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gggcccgaagg cgagatgaag ctgtagtctc gctggaagga ctagagggtta gaggagaccc 120
ccccgaaaca aaa                                     133

<210> 465
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF204177 region of
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<210> 466
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF204178 region of
        conserved sequence in 3' untranslated region

<400> 466
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ccccaaaaca aaa                                     133

<210> 467
<211> 133
<212> DNA
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<220>
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<210> 468  
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<220>  
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<210> 470  
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 ccccaaaaca aaa 133

<210> 471  
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 cccagacaaa aaaa 134  
  
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 cccagacaaa aaaa 134  
  
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<220>  
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 cccagacaaa aaa 133

<210> 477  
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<220>  
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<210> 478  
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<210> 479  
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<210> 480  
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<210> 481  
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<210> 482  
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<400> 482  
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 ccccgaaata aaa 133

<210> 483  
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<400> 483  
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<210> 484  
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<400> 484  
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<210> 485  
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<220>  
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<210> 486  
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<220>  
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<210> 487  
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<220>  
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 conserved sequence in 3' untranslated region

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<210> 488  
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 <212> DNA  
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<220>  
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 ccccgaaata aaa 133

<210> 489  
 <211> 133  
 <212> DNA  
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<220>  
 <223> Dengue virus type 2 strain M19197 region of conserved sequence in 3' untranslated region

<400> 489  
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 gggcccaagg tgagatgaag ctgtagtctc actggaagga ctagagggtta gaggagaccc 120  
 ccccaaaaca aaa 133

<210> 490  
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<220>  
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 ccccaaaaca aaa 133

<210> 491  
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<220>  
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<210> 492  
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<220>  
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<400> 492  
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<210> 493  
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<220>  
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<210> 494  
<211> 133  
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<220>  
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conserved sequence in 3' untranslated region

<400> 494  
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<210> 495  
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<210> 496  
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conserved sequence in 3' untranslated region

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<210> 497  
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<210> 498  
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<210> 504  
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<210> 508  
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 conserved sequence in 3' untranslated region

<400> 508  
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 cgcaaataaa 130

<210> 509  
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<220>  
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 conserved sequence in 3' untranslated region

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<210> 510  
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<220>  
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 conserved sequence in 3' untranslated region

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 cgcaaataaa 130

<210> 511  
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 <213> Dengue virus type 3  
  
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 <223> Dengue virus type 3 strain VR1256-3 region of  
       conserved sequence in 3' untranslated region  
  
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 cccgagcact gagggagct gtacctcctt gcaaaggact agagggtata ggagaccccc 120  
 cgcaaacaaa 130  
  
 <210> 512  
 <211> 130  
 <212> DNA  
 <213> Dengue virus type 3  
  
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 <223> Dengue virus type 3 strain VR1256-5 region of  
       conserved sequence in 3' untranslated region  
  
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 <210> 513  
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 <213> Dengue virus type 4  
  
 <220>  
 <223> Dengue virus type 4 strain M14931 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 513  
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 <210> 514  
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 <223> Dengue virus type 4 strain AF289029 region of  
       conserved sequence in 3' untranslated region  
  
 <400> 514  
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 aaagggggcc cgaagccagg aggaagctgt actcctggtg gaaggactag aggttagagg 120  
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<220>
<223> Dengue virus type 4 strain AF310150 region of
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<400> 515
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aggggggccc aagtcaggat gaagctgtac tcctgatgga agga 104

<210> 516
<211> 104
<212> DNA
<213> Dengue virus type 4

<220>
<223> Dengue virus type 4 strain AF310152 region of
        conserved sequence in 3' untranslated region

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aggggggccc aagtcaggat gaagctgtac tcctgatgga agga 104

<210> 517
<211> 136
<212> DNA
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<220>
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aggggggccc aagccaggag gaagctgtac tcctggtgga aggactagag gttagaggag 120
acccccccaa cacaaa 136

<210> 518
<211> 136
<212> DNA
<213> Dengue virus type 4

<220>
<223> Dengue virus type 4 strain AF326573 region of
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aggggggccc aagccaggag gaagctgtac tcctggtgga aggactagag gttagaggag 120
acccccccaa cacaaa 136

<210> 519
<211> 136
<212> DNA
<213> Dengue virus type 4

<220>
<223> Dengue virus type 4 strain AF326825 region of
        conserved sequence in 3' untranslated region

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<210> 592  
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<210> 593  
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<210> 594  
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<210> 596  
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<210> 597  
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<210> 599  
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<210> 600  
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<210> 601  
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<220>  
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